B' Cont synthase reductase polypeptide.

3. (Amended) The nucleic acid of claim 1, wherein said nucleic acid has the sequence of SEQ ID NO: 1, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, or SEQ ID NO: 47, or degenerate variants thereof, and wherein said nucleic acid encodes the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, or SEQ ID NO: 48.

Sub C1

4. (Amended) A substantially pure nucleic acid that hybridizes in 2X SSC medium at 40°C to a sequence found within SEQ ID NO: 1 or SEQ ID NO: 41, wherein said nucleic acid comprises a region complementary to a naturally-occurring mammalian methionine synthase reductase mutation or polymorphism.

B2

5. (Amended) The nucleic acid of claim 4, wherein said nucleic acid has a sequence complementary to at least 50% of at least 60 contiguous nucleotides of SEQ ID NO: 1 or SEQ ID NO: 41.

Add the following new claims 35-47.

35. (New) The nucleic acid of claim 4, wherein said mutation or polymorphism is an alteration relative to SEQ ID NO: 1 selected from the group consisting of:

a) the alteration from guanine to adenine at nucleotide position 66;

b) the alteration from guanine to adenine at nucleotide position 110;

c) the deletion of bases 1675-1678; and

d) the deletion of bases 1726-1728.

B3

36. (New) A substantially pure nucleic acid having a polynucleotide sequence that has at least 50% sequence identity to SEQ ID No.: 1 over the entire length of SEQ ID

Sub C2

No.: 1.

37. (New) The nucleic acid of claim 36, having a polynucleotide sequence that has at least 85% sequence identity to SEQ ID No.: 1 over the entire length of SEQ ID No.: 1.

38. (New) The nucleic acid of claim 37, having a polynucleotide sequence that has at least 95% sequence identity to SEQ ID No.: 1 over the entire length of SEQ ID No.: 1.

39. (New) The nucleic acid of claim 36, comprising a naturally-occurring mammalian methionine synthase reductase mutation or polymorphism.

B3

40. (New) The nucleic acid of claim 39, wherein said mutation or polymorphism is an alteration relative to SEQ ID NO: 1 selected from the group consisting of:

a) the alteration from guanine to adenine at nucleotide position 66;

b) the alteration from guanine to adenine at nucleotide position 110;

c) the deletion of bases 1675-1678; and

d) the deletion of bases 1726-1728.

B3 Cont

41. (New) A substantially pure nucleic acid having a polynucleotide sequence that has at least 50% sequence identity to the corresponding region of SEQ ID No.: 1, wherein said nucleic acid comprises a naturally-occurring mammalian methionine synthase reductase mutation or polymorphism.

Sub C3

42. (New) The nucleic acid of claim 41, having a polynucleotide sequence that has at least 85% sequence identity to the corresponding region of SEQ ID No.: 1.

43. (New) The nucleic acid of claim 42, having a polynucleotide sequence that has

at least 95% sequence identity to the corresponding region of SEQ ID No.: 1.

44. (New) The nucleic acid of claim 41, wherein said mutation or polymorphism is an alteration relative to SEQ ID NO: 1 selected from the group consisting of:

a) the alteration from guanine to adenine at nucleotide position 66;

b) the alteration from guanine to adenine at nucleotide position 110;

c) the deletion of bases 1675-1678; and

d) the deletion of bases 1726-1728.

45. (New) The nucleic acid of claim 1, 36, or 41, encoding a mammalian methionine synthase reductase polypeptide having at least 20-30% of the ability to catalyze the reductive methylation of methionine synthase-cob(II)alamin to generate methionine synthase-cob(III)alamin-CH3 as the methionine synthase reductase polypeptide of SEQ ID NO: 2.

46. (New) The nucleic acid of claim 45, encoding a mammalian methionine synthase reductase polypeptide having at least 55-75% of the ability to catalyze the reductive methylation of methionine synthase-cob(II)alamin to generate methionine synthase-cob(III)alamin-CH3 as the methionine synthase reductase polypeptide of SEQ ID NO: 2.

47. (New) The nucleic acid of claim 1, 36, or 41, encoding a mammalian methionine synthase reductase polypeptide that comprises a consensus binding site for one or more cofactors selected from the group consisting of FAD, FMN, and NADPH.